1   *Parameter estimation continued*
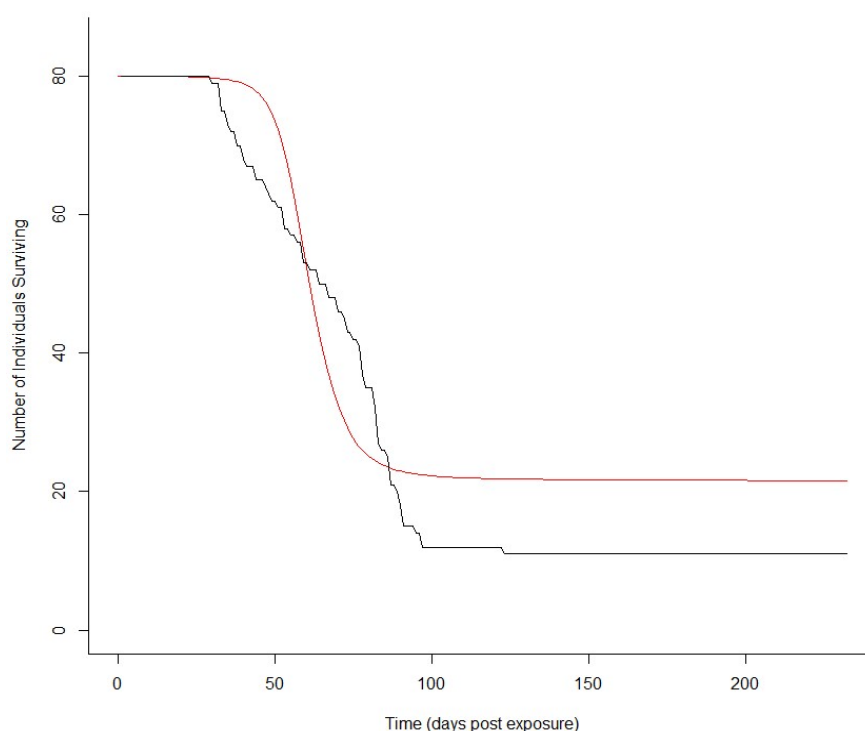
2   Experimental work has demonstrated several fish species are sensitive to *S. destruens*

3   infection at varying levels of virulence, including roach *Rutilus rutilus*, common carp *Cyprinus*

4   *carpio*, and sunbleak *Leucaspius delineatus*[1,2]. For all single host model outputs[3], there was

5   a range of possible values for each parameter that did not significantly alter the model

6   output's mean squared error (MSE) against the experimental data, suggesting that values

7   within this rangewere equally plausible. The nature of the experimental setups where hosts

8   are exposed to millions of spores restricted some parameters while leaving others with a

9   wider range of possible values (i.e. the model's uncertainty). This is an unavoidable limitation

10   of using empirical data, as experiments that overcome this difficulty are not possible.

11   Sensitivity analyses showed that this parameter selection did not significantly affect model

12   output.

13

14   Parameter values from the single host *L. delineatus* model were input into a two host model

15   including introduced reservoir host *Pseudorasbora parva* and *L. delineatus*, which was then

16   calibrated with experimental cohabitation data of these two species [1]. Even without direct

17   contact between species (they were kept in separate tanks), the transfer of infectious

18   propagules through the water column caused a severe *S. destruens* outbreak in *L.*

19   *delineatus* (Figure S1). The rate of spore release for *L. delineatus* found in the single host

20   model (350 per day) resulted in significantly faster mortalities in the two host system than

21   those observed, so this parameter was optimised in addition to the *P. parva* parameters,

22   testing for a value between 10 and 500. The value that resulted in the lowest MSE for the

23   two host model output was 120 spores per day, 34% of the value in the single host model.

24   This was expected as the experimental cohabitation did not artificially flood the model

25   system with spores, but only included spores naturally released from *P. parva*. This

26   adjustment was thus applied to the remaining species spore release values to simulate

27   naturally caused infections. The model was run for 100,000 iterations incorporating ± 25%

28   random variation in each parameter in each iteration to test for parameter sensitivity and

29   best fit values.

30

31   When all *P. parva* were assumed infected (100% disease prevalence), mortalities were

32   marginally higher than the experimental data (Welch two sample *t*-test: $t = 1.74$, d.f. = 464, *P*

33   = 0.083). This initial pathogen prevalence was systematically reduced by 10% until a best fit

34   was achieved at 10% prevalence. Therefore, 10% was selected as the initial prevalence

35   value, a conservative estimate compared with published values of 67%-74%[4]. However,

36   given that the pathogen was not detected in *P. parva* used in the cohabitation experiment,

37   this estimate was considered realistic and was further explored in the main text. The initial

38   pathogen prevalence was increased to 40% in the tested scenarios to discern the long-term

39   effects of pathogen prevalence. A non-zero recovery rate for *P. parva* allowed a better fit to

40   the experimental data, suggesting that reservoir host recovery and/or immunity plays a role

41   in the disease dynamics of *S. destruens*.

42

43   In the control experiments where there were no *P. parva* or infection, 6% of *L. delineatus*

44   died from causes unrelated to the pathogen. This corresponded to the discrepancy between

45   the observed and model mortality in Figure S1, where demographic rates were not included.

46   In the main text, this was addressed by incorporating natural birth and mortality rates for all

47   species, based on observed data.

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Figure axis labels: Number of Individuals Surviving (y-axis), Time (days post exposure) (x-axis)

58

59 **Supplementary Figure S1** Surviving population of *Leucaspius delineatus* when cohabited with introduced

60 reservoir host *Pseudorasbora parva.* The model (red) was calibrated using experimental cohabitation data[1]

61 shown in black.

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